The first full paragraph on page 14 has been amended as follows:

B2

Such variant forms of ORFV2-VEGF or NZ10 can be prepared by targeting non-essential regions of the ORFV2-VEGF or NZ10 polypeptide for modification. Other variant forms may be naturally made from related orf virus strains. These non-essential regions are expected to fall outside the strongly-conserved regions indicated in Figures 1A and 1B. In particular, the growth factors of the PDGF family, including VEGF, are dimeric, and VEGF, VEGF-B, VEGF-C, VEGF-D, ORFV2-VEGF, PlGF, PDGF-A and PDGF-B show complete conservation of eight cysteine residues in the N-terminal domains, *ie.* the PDGF-like domains (Olofsson *et al*, 1996; Joukov *et al*, 1996). These cysteines are thought to be involved in intra- and inter-molecular disulfide bonding. In addition there are further strongly, but not completely, conserved cysteine residues in the C-terminal domains. Loops 1, 2 and 3 of each subunit, which are formed by intra-molecular disulfide bonding, are involved in binding to the receptors for the PDGF/VEGF family of growth factors (Andersson *et al*: Growth Factors, 1995 12 159-164). As noted above, the cysteines conserved in previously known members of the VEGF family are also conserved in ORFV2-VEGF.

On Page 26, the paragraph between lines 13 and 27 have been amended as follows:

B3

Figures 1A and 1B show a comparative sequence alignment of the amino acid sequences of ORFV2-VEGF with other members of the VEGF family of growth factors. The deduced amino acid sequence of ORFV2-VEGF was aligned with the sequences of $VEGF_{121}$ (SEQ ID NO:3), $VEGF_{165}$ (SEQ ID NO:4), PlGF (SEQ ID NO:5), $VEGF\text{-}B_{167}$ (SEQ ID NO:6), and truncated sequences of VEGF-C (SEQ ID NO:7) and VEGF-D (SEQ ID NO:8). The residues which show identity with ORFV2-VEGF (SEQ ID NO:2) are boxed. The conserved cysteine residues of the cystine knot motif are indicated with an asterisk. The signal sequence as determined by N-terminal sequencing is indicated by the line above the sequence. The potential sites of N- and O-linked glycosylation are indicated by a bracket and dashed line respectively. The VEGF homology domain is indicated by arrows.

The paragraph bridging pages 29 and 30 has been amended as follows:

B4

Figures 1A and 1B show a comparative sequence alignment of the amino acid sequences of ORFV2-VEGF with other members of the VEGF family of growth factors.

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B